

SEQUENCE LISTING

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<120> SCREENING AND THERAPY FOR LYMPHATIC DISORDERS INVOLVING
THE FLT4 RECEPTOR TYROSINE KINASE (VEGFR-3)

<130> 28967/35255A

<140>

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<150> PCT/US99/06133

<151> 1999-03-26

<160> 28

<170> PatentIn Ver. 2.0

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 1155 1160 1165
 Leu Gly Asp Leu Leu Gln Gly Arg Gly Leu Gln Glu Glu Glu Val
 1170 1175 1180

Cys Met Ala Pro Arg Ser Ser Gln Ser Ser Glu Glu Gly Ser Phe Ser
185 1190 1195 1200

Gln Val Ser Thr Met Ala Leu His Ile Ala Gln Ala Asp Ala Glu Asp
1205 1210 1215

Ser Pro Pro Ser Leu Gln Arg His Ser Leu Ala Ala Arg Tyr Tyr Asn
1220 1225 1230

Trp Val Ser Phe Pro Gly Cys Leu Ala Arg Gly Ala Glu Thr Arg Gly
1235 1240 1245

Ser Ser Arg Met Lys Thr Phe Glu Glu Phe Pro Met Thr Pro Thr Thr
1250 1255 1260

Tyr Lys Gly Ser Val Asp Asn Gln Thr Asp Ser Gly Met Val Leu Ala
265 1270 1275 1280

Ser Glu Glu Phe Glu Gln Ile Glu Ser Arg His Arg Gln Glu Ser Gly
1285 1290 1295

Phe Ser Cys Lys Gly Pro Gly Gln Asn Val Ala Val Thr Arg Ala His
1300 1305 1310

Pro Asp Ser Gln Gly Arg Arg Arg Arg Pro Glu Arg Gly Ala Arg Gly
1315 1320 1325

Gly Gln Val Phe Tyr Asn Ser Glu Tyr Gly Glu Leu Ser Glu Pro Ser
1330 1335 1340

Glu Glu Asp His Cys Ser Pro Ser Ala Arg Val Thr Phe Phe Thr Asp
345 1350 1355 1360

Asn Ser Tyr

<210> 3

<211> 1997

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (352)..(1611)

<220>

<223> Human cDNA for prepro-VEGF-C

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ctcgcttcac ctgcggggct ccgaatgcgg ggagctcgga tgtccggttt cctgtgaggc 120

ttttacctga caccgcgcgc ctttccccgg cactggctgg gagggcgccc tgcaaagttg 180

ggaacgcgga gccccggacc cgctcccgcc gcctccggt cgcccagggg gggtcgccgg 240
gaggagcccc ggggagaggg accaggaggg gccgcggcc tcgcaggggc gcccgcgcc 300
ccaccctgc ccccgccagc ggaccggtcc cccacccccg gtccttcac c atg cac 357
Met His
1

ttg ctg ggc ttc ttc tct gtg gcg tgt tct ctg ctc gcc gct gcg ctg 405
Leu Leu Gly Phe Phe Ser Val Ala Cys Ser Leu Leu Ala Ala Ala Leu
5 10 15

ctc ccg ggt cct cgc gag gcg ccc gcc gcc gcc gcc gcc ttc gag tcc 453
Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala Ala Ala Phe Glu Ser
20 25 30

gga ctc gac ctc tcg gac gcg gag ccc gac gcg ggc gag gcc acg gct 501
Gly Leu Asp Leu Ser Asp Ala Glu Pro Asp Ala Gly Glu Ala Thr Ala
35 40 45 50

tat gca agc aaa gat ctg gag gag cag tta cgg tct gtg tcc agt gta 549
Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser Ser Val
55 60 65

gat gaa ctc atg act gta ctc tac cca gaa tat tgg aaa atg tac aag 597
Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met Tyr Lys
70 75 80

tgt cag cta agg aaa gga ggc tgg caa cat aac aga gaa cag gcc aac 645
Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn Arg Glu Gln Ala Asn
85 90 95

ctc aac tca agg aca gaa gag act ata aaa ttt gct gca gca cat tat 693
Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe Ala Ala Ala His Tyr
100 105 110

aat aca gag atc ttg aaa agt att gat aat gag tgg aga aag act caa 741
Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys Thr Gln
115 120 125 130

tgc atg cca cgg gag gtg tgt ata gat gtg ggg aag gag ttt gga gtc 789
Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe Gly Val
135 140 145

gcg aca aac acc ttc ttt aaa cct cca tgt gtg tcc gtc tac aga tgt 837
Ala Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Val Tyr Arg Cys
150 155 160

ggg ggt tgc tgc aat agt gag ggg ctg cag tgc atg aac acc agc acg 885
Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr Ser Thr
165 170 175

agc tac ctc agc aag acg tta ttt gaa att aca gtg cct ctc tct caa 933
Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu Ser Gln
180 185 190

ggc ccc aaa cca gta aca atc agt ttt gcc aat cac act tcc tgc cga	981
Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser Cys Arg	
195 200 205 210	
tgc atg tct aaa ctg gat gtt tac aga caa gtt cat tcc att att aga	1029
Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile Ile Arg	
215 220 225	
cgt tcc ctg cca gca aca cta cca cag tgt cag gca gcg aac aag acc	1077
Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn Lys Thr	
230 235 240	
tgc ccc acc aat tac atg tgg aat aat cac atc tgc aga tgc ctg gct	1125
Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile Cys Arg Cys Leu Ala	
245 250 255	
cag gaa gat ttt atg ttt tcc tcg gat gct gga gat gac tca aca gat	1173
Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly Asp Asp Ser Thr Asp	
260 265 270	
gga ttc cat gac atc tgt gga cca aac aag gag ctg gat gaa gag acc	1221
Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu Glu Thr	
275 280 285 290	
tgt cag tgt gtc tgc aga gcg ggg ctt cgg cct gcc agc tgt gga ccc	1269
Cys Gln Cys Val Cys Arg Ala Gly Leu Arg Pro Ala Ser Cys Gly Pro	
295 300 305	
cac aaa gaa cta gac aga aac tca tgc cag tgt gtc tgt aaa aac aaa	1317
His Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys Val Cys Lys Asn Lys	
310 315 320	
ctc ttc ccc agc caa tgt ggg gcc aac cga gaa ttt gat gaa aac aca	1365
Leu Phe Pro Ser Gln Cys Gly Ala Asn Arg Glu Phe Asp Glu Asn Thr	
325 330 335	
tgc cag tgt gta tgt aaa aga acc tgc ccc aga aat caa ccc cta aat	1413
Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro Leu Asn	
340 345 350	
cct gga aaa tgt gcc tgt gaa tgt aca gaa agt cca cag aaa tgc ttg	1461
Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser Pro Gln Lys Cys Leu	
355 360 365 370	
tta aaa gga aag aag ttc cac cac caa aca tgc agc tgt tac aga cgg	1509
Leu Lys Gly Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr Arg Arg	
375 380 385	
cca tgt acg aac cgc cag aag gct tgt gag cca gga ttt tca tat agt	1557
Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro Gly Phe Ser Tyr Ser	
390 395 400	
gaa gaa gtg tgt cgt tgt gtc cct tca tat tgg aaa aga cca caa atg	1605
Glu Glu Val Cys Arg Cys Val Pro Ser Tyr Trp Lys Arg Pro Gln Met	
405 410 415	

agc taa gattgtactg tttccagtt catcgatttt ctattatgga aaactgtgtt 1661
Ser

420

gccacagtag aactgtctgt gaacagagag acccttgtgg gtccatgcta acaaagacaa 1721
aagtctgtct ttcctgaacc atgtggataa ctttacagaa atggactgga gctcatctgc 1781
aaaaggcctc ttgtaaagac tggttttctg ccaatgacca aacagccaag attttcctct 1841
tgtgatttct ttaaaagaat gactatataa tttatttcca ctaaaaatat tgtttctgca 1901
ttcattttta tagcaacaac aattggtaaa actcactgtg atcaatattt ttatatcatg 1961
caaaatatgt ttaaaataaa atgaaaattg tattat 1997

<210> 4

<211> 419

<212> PRT

<213> Homo sapiens

<400> 4

Met His Leu Leu Gly Phe Phe Ser Val Ala Cys Ser Leu Leu Ala Ala
1 5 10 15

Ala Leu Leu Pro Gly Pro Arg Glu Ala Pro Ala Ala Ala Ala Ala Phe
20 25 30

Glu Ser Gly Leu Asp Leu Ser Asp Ala Glu Pro Asp Ala Gly Glu Ala
35 40 45

Thr Ala Tyr Ala Ser Lys Asp Leu Glu Glu Gln Leu Arg Ser Val Ser
50 55 60

Ser Val Asp Glu Leu Met Thr Val Leu Tyr Pro Glu Tyr Trp Lys Met
65 70 75 80

Tyr Lys Cys Gln Leu Arg Lys Gly Gly Trp Gln His Asn Arg Glu Gln
85 90 95

Ala Asn Leu Asn Ser Arg Thr Glu Glu Thr Ile Lys Phe Ala Ala Ala
100 105 110

His Tyr Asn Thr Glu Ile Leu Lys Ser Ile Asp Asn Glu Trp Arg Lys
115 120 125

Thr Gln Cys Met Pro Arg Glu Val Cys Ile Asp Val Gly Lys Glu Phe
130 135 140

Gly Val Ala Thr Asn Thr Phe Phe Lys Pro Pro Cys Val Ser Val Tyr
145 150 155 160

Arg Cys Gly Gly Cys Cys Asn Ser Glu Gly Leu Gln Cys Met Asn Thr
165 170 175

Ser Thr Ser Tyr Leu Ser Lys Thr Leu Phe Glu Ile Thr Val Pro Leu
180 185 190

Ser Gln Gly Pro Lys Pro Val Thr Ile Ser Phe Ala Asn His Thr Ser
195 200 205

Cys Arg Cys Met Ser Lys Leu Asp Val Tyr Arg Gln Val His Ser Ile
210 215 220

Ile Arg Arg Ser Leu Pro Ala Thr Leu Pro Gln Cys Gln Ala Ala Asn
225 230 235 240

Lys Thr Cys Pro Thr Asn Tyr Met Trp Asn Asn His Ile Cys Arg Cys
245 250 255

Leu Ala Gln Glu Asp Phe Met Phe Ser Ser Asp Ala Gly Asp Asp Ser
260 265 270

Thr Asp Gly Phe His Asp Ile Cys Gly Pro Asn Lys Glu Leu Asp Glu
275 280 285

Glu Thr Cys Gln Cys Val Cys Arg Ala Gly Leu Arg Pro Ala Ser Cys
290 295 300

Gly Pro His Lys Glu Leu Asp Arg Asn Ser Cys Gln Cys Val Cys Lys
305 310 315 320

Asn Lys Leu Phe Pro Ser Gln Cys Gly Ala Asn Arg Glu Phe Asp Glu
325 330 335

Asn Thr Cys Gln Cys Val Cys Lys Arg Thr Cys Pro Arg Asn Gln Pro
340 345 350

Leu Asn Pro Gly Lys Cys Ala Cys Glu Cys Thr Glu Ser Pro Gln Lys
355 360 365

Cys Leu Leu Lys Gly Lys Lys Phe His His Gln Thr Cys Ser Cys Tyr
370 375 380

Arg Arg Pro Cys Thr Asn Arg Gln Lys Ala Cys Glu Pro Gly Phe Ser
385 390 395 400

Tyr Ser Glu Glu Val Cys Arg Cys Val Pro Ser Tyr Trp Lys Arg Pro
405 410 415

Gln Met Ser

<210> 5

<211> 2029

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (411)..(1475)

<223> Human prepro-VEGF-D cDNA

<400> 5

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aactagaacc tgcggcatatc attggagaga tttttttaat tttctggaca tgaagtaaatt 120
ttagagtgtc ttctaatttc aggtagaaga catgtccacc ttctgattat ttttggagaa 180
cattttgatt tttttcatct ctctctcccc acccctaaga ttgtgcaaaa aaagcgtacc 240
ttgcctaatt gaaataattt cattggattt tgatcagaac tgattatttg gttttctgtg 300
tgaagttttg aggtttcaaa ctttccttct ggagaatgcc ttttgaaaca attttctcta 360
gctgcctgat gtcaactgct tagtaatcag tggatattga aatattcaaa atg tac 416
Met Tyr
1

aga gag tgg gta gtg gtg aat gtt ttc atg atg ttg tac gtc cag ctg 464
Arg Glu Trp Val Val Val Asn Val Phe Met Met Leu Tyr Val Gln Leu
5 10 15

gtg cag ggc tcc agt aat gaa cat gga cca gtg aag cga tca tct cag 512
Val Gln Gly Ser Ser Asn Glu His Gly Pro Val Lys Arg Ser Ser Gln
20 25 30

tcc aca ttg gaa cga tct gaa cag cag atc agg gct gct tct agt ttg 560
Ser Thr Leu Glu Arg Ser Glu Gln Gln Ile Arg Ala Ala Ser Ser Leu
35 40 45 50

gag gaa cta ctt cga att act cac tct gag gac tgg aag ctg tgg aga 608
Glu Glu Leu Leu Arg Ile Thr His Ser Glu Asp Trp Lys Leu Trp Arg
55 60 65

tgc agg ctg agg ctc aaa agt ttt acc agt atg gac tct cgc tca gca 656
Cys Arg Leu Arg Leu Lys Ser Phe Thr Ser Met Asp Ser Arg Ser Ala
70 75 80

tcc cat cgg tcc act agg ttt gcg gca act ttc tat gac att gaa aca 704
Ser His Arg Ser Thr Arg Phe Ala Ala Thr Phe Tyr Asp Ile Glu Thr
85 90 95

cta aaa gtt ata gat gaa gaa tgg caa aga act cag tgc agc cct aga 752
Leu Lys Val Ile Asp Glu Glu Trp Gln Arg Thr Gln Cys Ser Pro Arg
100 105 110

gaa acg tgc gtg gag gtg gcc agt gag ctg ggg aag agt acc aac aca 800
Glu Thr Cys Val Glu Val Ala Ser Glu Leu Gly Lys Ser Thr Asn Thr
115 120 125 130

ttc ttc aag ccc cct tgt gtg aac gtg ttc cga tgt ggt ggc tgt tgc 848
Phe Phe Lys Pro Pro Cys Val Asn Val Phe Arg Cys Gly Gly Cys Cys
135 140 145

aat gaa gag agc ctt atc tgt atg aac acc agc acc tcg tac att tcc	896
Asn Glu Glu Ser Leu Ile Cys Met Asn Thr Ser Thr Ser Tyr Ile Ser	
150 155 160	
aaa cag ctc ttt gag ata tca gtg cct ttg aca tca gta cct gaa tta	944
Lys Gln Leu Phe Glu Ile Ser Val Pro Leu Thr Ser Val Pro Glu Leu	
165 170 175	
gtg cct gtt aaa gtt gcc aat cat aca ggt tgt aag tgc ttg cca aca	992
Val Pro Val Lys Val Ala Asn His Thr Gly Cys Lys Cys Leu Pro Thr	
180 185 190	
gcc ccc cgc cat cca tac tca att atc aga aga tcc atc cag atc cct	1040
Ala Pro Arg His Pro Tyr Ser Ile Ile Arg Arg Ser Ile Gln Ile Pro	
195 200 205 210	
gaa gaa gat cgc tgt tcc cat tcc aag aaa ctc tgt cct att gac atg	1088
Glu Glu Asp Arg Cys Ser His Ser Lys Lys Leu Cys Pro Ile Asp Met	
215 220 225	
cta tgg gat agc aac aaa tgt aaa tgt gtt ttg cag gag gaa aat cca	1136
Leu Trp Asp Ser Asn Lys Cys Lys Cys Val Leu Gln Glu Glu Asn Pro	
230 235 240	
ctt gct gga aca gaa gac cac tct cat ctc cag gaa cca gct ctc tgt	1184
Leu Ala Gly Thr Glu Asp His Ser His Leu Gln Glu Pro Ala Leu Cys	
245 250 255	
ggg cca cac atg atg ttt gac gaa gat cgt tgc gag tgt gtc tgt aaa	1232
Gly Pro His Met Met Phe Asp Glu Asp Arg Cys Glu Cys Val Cys Lys	
260 265 270	
aca cca tgt ccc aaa gat cta atc cag cac ccc aaa aac tgc agt tgc	1280
Thr Pro Cys Pro Lys Asp Leu Ile Gln His Pro Lys Asn Cys Ser Cys	
275 280 285 290	
ttt gag tgc aaa gaa agt ctg gag acc tgc tgc cag aag cac aag cta	1328
Phe Glu Cys Lys Glu Ser Leu Glu Thr Cys Cys Gln Lys His Lys Leu	
295 300 305	
ttt cac cca gac acc tgc agc tgt gag gac aga tgc ccc ttt cat acc	1376
Phe His Pro Asp Thr Cys Ser Cys Glu Asp Arg Cys Pro Phe His Thr	
310 315 320	
aga cca tgt gca agt ggc aaa aca gca tgt gca aag cat tgc cgc ttt	1424
Arg Pro Cys Ala Ser Gly Lys Thr Ala Cys Ala Lys His Cys Arg Phe	
325 330 335	
cca aag gag aaa agg gct gcc cag ggg ccc cac agc cga aag aat cct	1472
Pro Lys Glu Lys Arg Ala Ala Gln Gly Pro His Ser Arg Lys Asn Pro	
340 345 350	
tga ttcagcgttc caagttcccc atccctgtca tttttaacag catgctgctt	1525

tgccaagttg ctgtcactgt ttttttccca ggtgttaaaa aaaaaatcca ttttacacag 1585
caccacagtg aatccagacc aaccttccat tcacaccagc taaggagtcc ctggttcatt 1645
gatggatgtc ttctagctgc agatgcctct gcgcaccaag gaatggagag gaggggaccc 1705
atgtaatcct tttgttttagt tttgtttttg ttttttggtg aatgagaaaag gtgtgctggt 1765
catggaatgg caggtgtcat atgactgatt actcagagca gatgaggaaa actgtagtct 1825
ctgagtcctt tgctaatcgc aactcttggtg aattattctg attctttttt atgcagaatt 1885
tgattcgtat gatcagtact gactttctga ttactgtcca gcttatagtc ttccagttaa 1945
atgaactacc atctgatgtt tcatatttaa gtgtatttaa agaaaataaa caccattatt 2005
caagccaaaa aaaaaaaaaa aaaa 2029

<210> 6
<211> 354
<212> PRT
<213> Homo sapiens

<400> 6

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20 25 30

Ser Gln Ser Thr Leu Glu Arg Ser Glu Gln Gln Ile Arg Ala Ala Ser
35 40 45

Ser Leu Glu Glu Leu Leu Arg Ile Thr His Ser Glu Asp Trp Lys Leu
50 55 60

Trp Arg Cys Arg Leu Arg Leu Lys Ser Phe Thr Ser Met Asp Ser Arg
65 70 75 80

Ser Ala Ser His Arg Ser Thr Arg Phe Ala Ala Thr Phe Tyr Asp Ile
85 90 95

Glu Thr Leu Lys Val Ile Asp Glu Glu Trp Gln Arg Thr Gln Cys Ser
100 105 110

Pro Arg Glu Thr Cys Val Glu Val Ala Ser Glu Leu Gly Lys Ser Thr
115 120 125

Asn Thr Phe Phe Lys Pro Pro Cys Val Asn Val Phe Arg Cys Gly Gly
130 135 140

Cys Cys Asn Glu Glu Ser Leu Ile Cys Met Asn Thr Ser Thr Ser Tyr
145 150 155 160

Ile	Ser	Lys	Gln	Leu	Phe	Glu	Ile	Ser	Val	Pro	Leu	Thr	Ser	Val	Pro			
				165					170					175				
Glu	Leu	Val	Pro	Val	Lys	Val	Ala	Asn	His	Thr	Gly	Cys	Lys	Cys	Leu			
			180					185					190					
Pro	Thr	Ala	Pro	Arg	His	Pro	Tyr	Ser	Ile	Ile	Arg	Arg	Ser	Ile	Gln			
		195					200					205						
Ile	Pro	Glu	Glu	Asp	Arg	Cys	Ser	His	Ser	Lys	Lys	Leu	Cys	Pro	Ile			
		210				215					220							
Asp	Met	Leu	Trp	Asp	Ser	Asn	Lys	Cys	Lys	Cys	Val	Leu	Gln	Glu	Glu			
225					230					235				240				
Asn	Pro	Leu	Ala	Gly	Thr	Glu	Asp	His	Ser	His	Leu	Gln	Glu	Pro	Ala			
				245					250					255				
Leu	Cys	Gly	Pro	His	Met	Met	Phe	Asp	Glu	Asp	Arg	Cys	Glu	Cys	Val			
			260					265					270					
Cys	Lys	Thr	Pro	Cys	Pro	Lys	Asp	Leu	Ile	Gln	His	Pro	Lys	Asn	Cys			
		275					280					285						
Ser	Cys	Phe	Glu	Cys	Lys	Glu	Ser	Leu	Glu	Thr	Cys	Cys	Gln	Lys	His			
		290				295					300							
Lys	Leu	Phe	His	Pro	Asp	Thr	Cys	Ser	Cys	Glu	Asp	Arg	Cys	Pro	Phe			
305					310					315				320				
His	Thr	Arg	Pro	Cys	Ala	Ser	Gly	Lys	Thr	Ala	Cys	Ala	Lys	His	Cys			
				325					330					335				
Arg	Phe	Pro	Lys	Glu	Lys	Arg	Ala	Ala	Gln	Gly	Pro	His	Ser	Arg	Lys			
			340					345					350					

Asn Pro

<210> 7

<211> 17

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 7

tcaccatcga tccaagc

<210> 8

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 8

agttctgcgt gagccgag

18

<210> 9

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 9

caggacgggg tgacttga

18

<210> 10

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 10

gccacggcct gtctactg

18

<210> 11

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 11

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18

<210> 12

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: primer

<400> 12

ggcaacagct ggatgtca

18

<210> 13
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 13
ctgtgagggc gtgggagt 18

<210> 14
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 14
gtcctttgag ccactgga 18

<210> 15
<211> 21
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 15
cacacgtcat cgacaccggt g 21

<210> 16
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: primer

<400> 16
ggcaacagct ggatgtca 18

<210> 17
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:

oligonucleotide

<400> 17

cctgagtatc tcccgcgtcg c

21

<210> 18

<211> 21

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:
oligonucleotide

<400> 18

ggtgcctccc tgtaccctgg g

21

<210> 19

<211> 1363

<212> PRT

<213> Mus musculus

<400> 19

Met Gln Pro Gly Ala Ala Leu Asn Leu Arg Leu Trp Leu Cys Leu Gly
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Leu Leu Gln Gly Leu Ala Asn Gly Tyr Ser Met Thr Pro Pro Thr Leu
20 25 30

Asn Ile Thr Glu Asp Ser Tyr Val Ile Asp Thr Gly Asp Ser Leu Ser
35 40 45

Ile Ser Cys Arg Gly Gln His Pro Leu Glu Trp Thr Trp Pro Gly Ala
50 55 60

Gln Glu Val Leu Thr Thr Gly Gly Lys Asp Ser Glu Asp Thr Arg Val
65 70 75 80

Val His Asp Cys Glu Gly Thr Glu Ala Arg Pro Tyr Cys Lys Val Leu
85 90 95

Leu Leu Ala Gln Thr His Ala Asn Asn Thr Gly Ser Tyr His Cys Tyr
100 105 110

Tyr Lys Tyr Ile Lys Ala Arg Ile Glu Gly Thr Thr Ala Ala Ser Thr
115 120 125

Tyr Val Phe Val Arg Asp Phe Lys His Pro Phe Ile Asn Lys Pro Asp
130 135 140

Thr Leu Leu Val Asn Arg Lys Asp Ser Met Trp Val Pro Cys Leu Val
145 150 155 160

Ser Ile Pro Gly Leu Asn Ile Thr Leu Arg Ser Gln Ser Ser Ala Leu
165 170 175

His Pro Asp Gly Gln Glu Val Leu Trp Asp Asp Arg Arg Gly Met Arg
180 185 190

Val Pro Thr Gln Leu Leu Arg Asp Ala Leu Tyr Leu Gln Cys Glu Thr
195 200 205

Thr Trp Gly Asp Gln Asn Phe Leu Ser Asn Leu Phe Val Val His Ile
210 215 220

Thr Gly Asn Glu Leu Tyr Asp Ile Gln Leu Tyr Pro Lys Lys Ser Met
225 230 235 240

Glu Leu Leu Val Gly Glu Lys Leu Val Leu Asn Cys Thr Val Trp Ala
245 250 255

Glu Phe Asp Ser Gly Val Thr Phe Asp Trp Asp Tyr Pro Gly Lys Gln
260 265 270

Ala Glu Arg Ala Lys Trp Val Pro Glu Arg Arg Ser Gln Gln Thr His
275 280 285

Thr Glu Leu Ser Ser Ile Leu Thr Ile His Asn Val Ser Gln Asn Asp
290 295 300

Leu Gly Pro Tyr Val Cys Glu Ala Asn Asn Gly Ile Gln Arg Phe Arg
305 310 315 320

Glu Ser Thr Glu Val Ile Val His Glu Lys Pro Phe Ile Ser Val Glu
325 330 335

Trp Leu Lys Gly Pro Val Leu Glu Ala Thr Ala Gly Asp Glu Leu Val
340 345 350

Lys Leu Pro Val Lys Leu Ala Ala Tyr Pro Pro Pro Glu Phe Gln Trp
355 360 365

Tyr Lys Asp Arg Lys Ala Val Thr Gly Arg His Asn Pro His Ala Leu
370 375 380

Val Leu Lys Glu Val Thr Glu Ala Ser Ala Gly Val Tyr Thr Leu Ala
385 390 395 400

Leu Trp Asn Ser Ala Ala Gly Leu Arg Gln Asn Ile Ser Leu Glu Leu
405 410 415

Val Val Asn Val Pro Pro His Ile His Glu Lys Glu Ala Ser Ser Pro
420 425 430

Ser Ile Tyr Ser Arg His Ser Arg Gln Thr Leu Thr Cys Thr Ala Tyr
435 440 445

Gly Val Pro Gln Pro Leu Ser Val Gln Trp His Trp Arg Pro Trp Thr
450 455 460

Pro Cys Lys Thr Phe Ala Gln Arg Ser Leu Arg Arg Arg Gln Gln Arg
465 470 475 480

Asp Gly Met Pro Gln Cys Arg Asp Trp Lys Glu Val Thr Thr Gln Asp
485 490 495

Ala Val Asn Pro Ile Glu Ser Leu Asp Ser Trp Thr Glu Phe Val Glu
500 505 510

Gly Lys Asn Lys Thr Val Ser Lys Leu Val Ile Gln Asp Ala Asn Val
515 520 525

Ser Ala Met Tyr Lys Cys Val Val Val Asn Lys Val Gly Gln Asp Glu
530 535 540

Arg Leu Ile Tyr Phe Tyr Val Thr Thr Ile Pro Asp Gly Phe Ser Ile
545 550 555 560

Glu Ser Glu Pro Ser Glu Asp Pro Leu Glu Gly Gln Ser Val Arg Leu
565 570 575

Ser Cys Arg Ala Asp Asn Tyr Thr Tyr Glu His Leu Arg Trp Tyr Arg
580 585 590

Leu Asn Leu Ser Thr Leu His Asp Ala Gln Gly Asn Pro Leu Leu Leu
595 600 605

Asp Cys Lys Asn Val His Leu Phe Ala Thr Pro Leu Glu Ala Asn Leu
610 615 620

Glu Glu Ala Glu Pro Gly Ala Arg His Ala Thr Leu Ser Leu Asn Ile
625 630 635 640

Pro Arg Val Ala Pro Glu Asp Glu Gly Asp Tyr Val Cys Glu Val Gln
645 650 655

Asp Arg Arg Ser Gln Asp Lys His Cys His Lys Lys Tyr Leu Ser Val
660 665 670

Gln Ala Leu Glu Ala Pro Arg Leu Thr Gln Asn Leu Thr Asp Leu Leu
675 680 685

Val Asn Val Ser Asp Ser Leu Glu Met Arg Cys Pro Val Ala Gly Ala
690 695 700

His Val Pro Ser Ile Val Trp Tyr Lys Asp Glu Arg Leu Leu Glu Lys
705 710 715 720

Glu Ser Gly Ile Asp Leu Ala Asp Ser Asn Gln Arg Leu Ser Ile Gln
725 730 735

Arg	Val	Arg	Glu	Glu	Asp	Ala	Gly	Arg	Tyr	Leu	Cys	Ser	Val	Cys	Asn	740	745	750
Ala	Lys	Gly	Cys	Val	Asn	Ser	Ser	Ala	Ser	Val	Ala	Val	Glu	Gly	Ser	755	760	765
Glu	Asp	Lys	Gly	Ser	Met	Glu	Ile	Val	Ile	Leu	Ile	Gly	Thr	Gly	Val	770	775	780
Ile	Ala	Val	Phe	Phe	Trp	Val	Leu	Leu	Leu	Leu	Ile	Phe	Cys	Asn	Met	785	790	795
Lys	Arg	Pro	Ala	His	Ala	Asp	Ile	Lys	Thr	Gly	Tyr	Leu	Ser	Ile	Ile	805	810	815
Met	Asp	Pro	Gly	Glu	Val	Pro	Leu	Glu	Glu	Gln	Cys	Glu	Tyr	Leu	Ser	820	825	830
Tyr	Asp	Ala	Ser	Gln	Trp	Glu	Phe	Pro	Arg	Glu	Arg	Leu	His	Leu	Gly	835	840	845
Arg	Val	Leu	Gly	His	Gly	Ala	Phe	Gly	Lys	Val	Val	Glu	Ala	Ser	Ala	850	855	860
Phe	Gly	Ile	Asn	Lys	Gly	Ser	Ser	Cys	Asp	Thr	Val	Ala	Val	Lys	Met	865	870	875
Leu	Lys	Glu	Gly	Ala	Thr	Ala	Ser	Glu	His	Arg	Ala	Leu	Met	Ser	Glu	885	890	895
Leu	Lys	Ile	Leu	Ile	His	Ile	Gly	Asn	His	Leu	Asn	Val	Val	Asn	Leu	900	905	910
Leu	Gly	Ala	Cys	Thr	Lys	Pro	Asn	Gly	Pro	Leu	Met	Val	Ile	Val	Glu	915	920	925
Phe	Cys	Lys	Tyr	Gly	Asn	Leu	Ser	Asn	Phe	Leu	Arg	Val	Lys	Arg	Asp	930	935	940
Thr	Phe	Asn	Pro	Tyr	Ala	Glu	Lys	Ser	Pro	Glu	Gln	Arg	Arg	Arg	Phe	945	950	955
Arg	Ala	Met	Val	Glu	Gly	Ala	Lys	Ala	Asp	Arg	Arg	Arg	Pro	Gly	Ser	965	970	975
Ser	Asp	Arg	Ala	Leu	Phe	Thr	Arg	Phe	Leu	Met	Gly	Lys	Gly	Ser	Ala	980	985	990
Arg	Arg	Ala	Pro	Leu	Val	Gln	Glu	Ala	Glu	Asp	Leu	Trp	Leu	Ser	Pro	995	1000	1005
Leu	Thr	Met	Glu	Asp	Leu	Val	Cys	Tyr	Ser	Phe	Gln	Val	Ala	Arg	Gly	1010	1015	1020

Met Glu Phe Leu Ala Ser Arg Lys Cys Ile His Arg Asp Leu Ala Ala
1025 1030 1035 1040

Arg Asn Ile Leu Leu Ser Glu Ser Asp Ile Val Lys Ile Cys Asp Phe
1045 1050 1055

Gly Leu Ala Arg Asp Ile Tyr Lys Asp Pro Asp Tyr Val Arg Lys Gly
1060 1065 1070

Ser Ala Arg Leu Pro Leu Lys Trp Met Ala Pro Glu Ser Ile Phe Asp
1075 1080 1085

Lys Val Tyr Thr Thr Gln Ser Asp Val Trp Ser Phe Gly Val Leu Leu
1090 1095 1100

Trp Glu Ile Phe Ser Leu Gly Ala Ser Pro Tyr Pro Gly Val Gln Ile
1105 1110 1115 1120

Asn Glu Glu Phe Cys Gln Arg Leu Lys Asp Gly Thr Arg Met Arg Ala
1125 1130 1135

Pro Glu Leu Ala Thr Pro Ala Ile Arg His Ile Met Gln Ser Cys Trp
1140 1145 1150

Ser Gly Asp Pro Lys Ala Arg Pro Ala Phe Ser Asp Leu Val Glu Ile
1155 1160 1165

Leu Gly Asp Leu Leu Gln Gly Gly Gly Trp Gln Glu Glu Glu Glu
1170 1175 1180

Arg Met Ala Leu His Ser Ser Gln Ser Ser Glu Glu Asp Gly Phe Met
1185 1190 1195 1200

Gln Ala Ser Thr Thr Ala Leu His Ile Thr Glu Ala Asp Ala Asp Asp
1205 1210 1215

Ser Pro Pro Ser Met His Cys His Ser Leu Ala Ala Arg Tyr Tyr Asn
1220 1225 1230

Cys Val Ser Phe Pro Gly Arg Leu Ala Arg Gly Thr Lys Thr Pro Gly
1235 1240 1245

Ser Ser Arg Met Lys Thr Phe Glu Glu Leu Pro Met Thr Pro Thr Thr
1250 1255 1260

Tyr Lys Ala Ser Met Asp Asn Gln Thr Asp Ser Gly Met Val Leu Ala
1265 1270 1275 1280

Ser Glu Glu Phe Glu Glu Leu Glu Ser Arg His Arg Pro Glu Gly Ser
1285 1290 1295

Phe Ser Cys Lys Gly Pro Gly Gln His Met Asp Ile Pro Arg Gly His
1300 1305 1310

Pro Asp Pro Gln Gly Arg Arg Arg Pro Thr Gln Gly Ala Gln Gly
1315 1320 1325

Gly Lys Val Phe Tyr Asn Asn Glu Tyr Gly Glu Val Ser Gln Pro Cys
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Thr Glu Gly Asp Cys Cys Pro Ser Ala Gly Ser Thr Phe Phe Ala Asp
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Ser Ser Tyr

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oligonucleotide

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21

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18

<210> 25

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<212> DNA

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<223> Description of Artificial Sequence: primer

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18